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## SEQUENCE LISTING

&lt;110&gt; Nordlund, Henri Rainer et al.

&lt;120&gt; Avidin mutants

&lt;130&gt; BP110588

&lt;160&gt; 29

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Gallus gallus

&lt;400&gt; 1

Met Val His Ala Thr Ser Pro Leu Leu Leu Leu Leu Leu Ser Leu  
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Ala Leu Val Ala Pro Gly Leu Ser Ala Arg Lys Cys Ser Leu Thr Gly  
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Lys Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn  
 35 40 45

Ser Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr  
 50 55 60

Ser Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile  
 65 70 75 80

Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe  
 85 90 95

Ser Glu Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn  
 100 105 110

Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn  
 115 120 125

Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe  
 130 135 140

Thr Arg Leu Arg Thr Gln Lys Glu  
 145 150

&lt;210&gt; 2

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Gallus gallus

&lt;400&gt; 2

Met Val His Ala Thr Ser Pro Leu Leu Leu Leu Leu Leu Ser Leu  
 1 5 10 15

Ala Leu Val Ala Pro Gly Leu Ser Ala Arg Lys Arg Thr Gln Pro Thr  
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Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe  
 35 40 45

Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr  
 50 55 60

Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys  
 65 70 75 80

Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys  
 85 90 95

Glu Gly Gly Ser Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys  
 100 105 110

Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser  
 115 120 125

Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser  
 130 135 140

Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn  
 145 150 155 160

Lys Ser Gly Gly Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp  
 165 170 175

Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser  
 180 185 190

Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn  
 195 200 205

Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gly Gly Ser Gly Gly Ser  
 210 215 220

Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser  
 225 230 235 240

Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr  
 245 250 255

Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro  
 260 265 270

Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe  
 275 280 285

Gly Phe Thr Val Asn Trp Lys Phe Ser Glu  
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<400> 3

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23

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<400> 23  
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<210> 24  
 <211> 581  
 <212> PRT  
 <213> Gallus gallus

<400> 24

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Phe	Gly	Phe	Thr	Val	Asn	Trp	Lys	Phe	Ser	Glu	Ser	Thr	Thr	Val	Phe
	35						40					45			
Thr	Gly	Gln	Cys	Phe	Ile	Asp	Arg	Asn	Gly	Lys	Glu	Val	Leu	Lys	Thr
	50					55					60				
Met	Trp	Leu	Leu	Arg	Ser	Ser	Val	Asn	Asp	Ile	Gly	Asp	Asp	Trp	Lys
	65					70					75				80
Ala	Thr	Arg	Val	Gly	Ile	Asn	Ile	Phe	Thr	Arg	Leu	Arg	Thr	Gln	Lys
				85					90					95	
Glu	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Arg	Lys	Cys	Ser	Leu	Thr	Gly	Lys
			100					105						110	
Trp	Thr	Asn	Asp	Leu	Gly	Ser	Asn	Met	Thr	Ile	Gly	Ala	Val	Asn	Ser
		115					120					125			
Arg	Gly	Glu	Phe	Thr	Gly	Thr	Tyr	Ile	Thr	Ala	Val	Thr	Ala	Thr	Ser
	130					135					140				
Asn	Glu	Ile	Lys	Glu	Ser	Pro	Leu	His	Gly	Thr	Gln	Asn	Thr	Ile	Asn
	145					150					155				160
Lys	Ser	Gly	Gly	Ser	Thr	Thr	Val	Phe	Thr	Gly	Gln	Cys	Phe	Ile	Asp
				165					170					175	
Arg	Asn	Gly	Lys	Glu	Val	Leu	Lys	Thr	Met	Trp	Leu	Leu	Arg	Ser	Ser
			180					185					190		
Val	Asn	Asp	Ile	Gly	Asp	Asp	Trp	Lys	Ala	Thr	Arg	Val	Gly	Ile	Asn
		195					200					205			
Ile	Phe	Thr	Arg	Leu	Arg	Thr	Gln	Lys	Glu	Gly	Gly	Ser	Gly	Gly	Ser
	210					215					220				
Ala	Arg	Lys	Cys	Ser	Leu	Thr	Gly	Lys	Trp	Thr	Asn	Asp	Leu	Gly	Ser
	225					230					235				240
Asn	Met	Thr	Ile	Gly	Ala	Val	Asn	Ser	Arg	Gly	Glu	Phe	Thr	Gly	Thr
				245					250					255	
Tyr	Ile	Thr	Ala	Val	Thr	Ala	Thr	Ser	Asn	Glu	Ile	Lys	Glu	Ser	Pro
			260					265					270		

Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe  
 275 280 285  
 Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Gly Gly Ser Gly Ser Gly  
 290 295 300  
 Ser Gly Ser Gly Ser Gly Arg Thr Gln Pro Thr Phe Gly Phe Thr Val  
 305 310 315 320  
 Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe Thr Gly Gln Cys Phe  
 325 330 335  
 Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg  
 340 345 350  
 Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly  
 355 360 365  
 Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gly Gly Ser Gly  
 370 375 380  
 Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu  
 385 390 395 400  
 Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr  
 405 410 415  
 Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu  
 420 425 430  
 Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys Ser Gly Gly Ser  
 435 440 445  
 Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu  
 450 455 460  
 Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly  
 465 470 475 480  
 Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu  
 485 490 495  
 Arg Thr Gln Lys Glu Gly Gly Ser Gly Gly Ser Ala Arg Lys Cys Ser  
 500 505 510



Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly  
 515 520 525

Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val  
 530 535 540

Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln  
 545 550 555 560

Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn  
 565 570 575

Trp Lys Phe Ser Glu  
 580

<210> 25  
 <211> 1746  
 <212> DNA  
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 <221> DNA  
 <223> DNA sequence which codes for scAvd of SEQ ID NO 24

<400> 25  
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 ttttcagagt ccaccactgt cttcacgggc cagtgttca tagacaggaa tgggaaggag 180  
 gtcctgaaga ccatgtggct gctgcgggtca agtggttaatg acattggtga tgactggaaa 240  
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 ggaggctccg ccagaaagtg ctgctgact gggaaatgga ccaacgatct gggctccaac 360  
 atgaccatcg gggctgtgaa cagcagaggt gaattcacag gcacctacat cacagccgta 420  
 acagccacat caaatgagat caaagagtca cactgcatg ggacacaaaa caccatcaac 480  
 aagtccggcg gatccaccac tgtcttcacg ggccagtgt tcatagacag gaatgggaag 540  
 gaggtcctga agaccatgtg gctgctgcgg tcaagtgtta atgacattgg tgatgactgg 600  
 aaagctacca gggtcggcat caacatcttc actcgctgc gcacacagaa ggagggaggc 660  
 tccggaggct ccgccagaaa gtgctcgctg actgggaaat ggaccaacga tctgggctcc 720  
 aacatgacca tcggggctgt gaacagcaga ggtgaattca caggcaccta catcacagcc 780  
 gtaacagcca catcaaatga gatcaaagag tcaccactgc atgggacaca aaacaccatc 840  
 aacaagagga cccagcccac ctttggttc accgtcaatt ggaagttttc agagggagggt 900  
 tccggatcgg gatccggctc tggcagcggc aggaccacgc ccacctttgg cttcaccgtc 960

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aattggaagt tttcagagtc caccactgtc ttcacgggcc agtgcttcat agacaggaat 1020
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gactggaaag ctaccagggt cggcatcaac atcttctact gcctgcgcac acagaaggag 1140
ggaggctccg gaggtccgc cagaaagtgc tcgctgactg ggaaatggac caacgatctg 1200
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acagccgtaa cagccacatc aaatgagatc aaagagtcac cactgcatgg gacacaaaac 1320
accatcaaca agtccggcgg atccaccact gtcttcacgg gccagtgctt catagacagg 1380
aatgggaagg aggtcctgaa gaccatgtgg ctgctgcggt caagtgttaa tgacattggt 1440
gatgactgga aagctaccag ggtcggcatc aacatcttca ctgcctgcg cacacagaag 1500
gagggaggct ccggaggctc cgccagaaag tgctcgctga ctgggaaatg gaccaacgat 1560
ctgggctcca acatgaccat cggggctgtg aacagcagag gtgaattcac aggcacctac 1620
atcacagccg taacagccac atcaaatgag atcaaagagt caccactgca tgggacacaa 1680
aacaccatca acaagaggac ccagcccacc tttggcttca ccgtcaattg gaagttttca 1740
gagtga 1746

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<210> 26
<211> 897
<212> DNA
<213> Gallus gallus
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<223> DNA sequence which codes for dcAvd of SEQ ID 2

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ttttcagagt ccaccactgt cttcacgggc cagtgttca tagacaggaa tgggaaggag 180
gtcctgaaga ccatgtggct gctgcgggtc agtggttaatg acattggtga tgactggaaa 240
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aagtccggcg gatccaccac tgtcttcacg ggccagtgtc tcatagacag gaatgggaag 540
gaggtcctga agaccatgtg gctgctgcgg tcaagtgtta atgacattgg tgatgactgg 600
aaagctacca gggtcggcat caacatcttc actgcctgc gcacacagaa ggaggagggc 660

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tccggaggct ccgccagaaa gtgctcgctg actgggaaat ggaccaacga tctgggctcc 720  
 aacatgacca tcggggctgt gaacagcaga ggtgaattca caggcaccta catcacagcc 780  
 gtaacagcca catcaaatga gatcaaagag tcaccactgc atgggacaca aaacaccatc 840  
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 <223> primer cp34\_C1

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<210> 28  
 <211> 290  
 <212> PRT  
 <213> Gallus gallus

<400> 28

Met Asn Lys Pro Ser Lys Phe Ala Leu Pro Leu Ala Phe Ala Ala Val  
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 20 25 30

Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe Thr Gly Gln  
 35 40 45

Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu  
 50 55 60

Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg  
 65 70 75 80

Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gly Gly  
 85 90 95

Ser Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn  
 100 105 110

Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu  
 115 120 125

Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile

130                      135                      140  
 Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys Ser Gly  
 145                      150                      155                      160  
 Gly Ser Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys  
                     165                      170                      175  
 Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu  
                     180                      185                      190  
 Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys  
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 Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile  
                     210                      215                      220  
 Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg  
 225                      230                      235                      240  
 Leu Arg Thr Gln Lys Glu Gly Gly Ser Gly Gly Ser Ala Arg Lys Cys  
                     245                      250                      255  
 Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile  
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 Val Thr  
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 gtcggcatca acatcttcac tcgcctgcgc acacagaagg agggaggctc cggaggctcc      300  
 gccagaaagt gctcgctgac tgggaaatgg accaacgatc tgggctccaa catgaccatc      360

ggggctgtga acagcagagg tgaattcaca ggcacctaca tcacagccgt aacagccaca 420  
tcaaattgaga tcaaagagtc accactgcat gggacacaaa acaccatcaa caagtccggc 480  
ggatccaaag agtcaccact gcatgggaca caaaacacca tcaacaagag gaccagccc 540  
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tgcttcatag acaggaatgg gaaggaggtc ctgaagacca tgtggctgct gcggtcaagt 660  
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ctgcgcacac agaaggaggg aggctccgga ggctccgcca gaaagtgctc gctgactggg 780  
aaatggacca acgatctggg ctccaacatg accatcgggg ctgtgaacag cagaggtgaa 840  
ttcacaggca cctacatcac agccgtaaca taa 873

